



RAW SEQUENCE LISTING

DATE: 08/22/2002

PATENT APPLICATION: US/09/637,302C

TIME: 16:34:07

Input Set : A:\TSRI7102Seq-list.TXT

Output Set: N:\CRF3\08222002\I637302C.raw

ENTERED

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4 <110> APPLICANT: HOOD, John
5     ELICEIRI, Brian
6     CHERESH, David
8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
9     MODULATION OF ANGIOGENESIS USING TYROSINE KINASE RAF AND RAS
12 <130> FILE REFERENCE: TSRI 710.2
14 <140> CURRENT APPLICATION NUMBER: US 09/637,302C
15 <141> CURRENT FILING DATE: 2000-08-11
17 <150> PRIOR APPLICATION NUMBER: US 60/148,924
18 <151> PRIOR FILING DATE: 1999-08-13
20 <150> PRIOR APPLICATION NUMBER: US 60/215,951
21 <151> PRIOR FILING DATE: 2000-07-05
23 <160> NUMBER OF SEQ ID NOS: 7
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28 <211> LENGTH: 2977
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (130)...(2073)
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38 tgccgccgaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa 120
39 gctgcatca atg gag cac ata cag gga gct tgg aag acg atc agc aat ggt 171
40     Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly
41         1             5             10
43 ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct 219
44 Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro
45 15             20             25             30
47 aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc 267
48 Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly
49             35             40             45
51 aaa ctc aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg 315
52 Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu
53             50             55             60
55 ccg aac aag caa aga aca gtg gtc aat gtg cga aat gga atg agc ttg 363
56 Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu
57             65             70             75
59 cat gac tgc ctt atg aaa gca ctc aag gtg agg ggc ctg caa cca gag 411
60 His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu
61             80             85             90
63 tgc tgt gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca 459

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64	Cys	Cys	Ala	Val	Phe	Arg	Leu	Leu	His	Glu	His	Lys	Gly	Lys	Lys	Ala	
65	95					100					105					110	
67	cgc	tta	gat	tgg	aat	act	gat	gct	gcg	tct	ttg	att	gga	gaa	gaa	ctt	507
68	Arg	Leu	Asp	Trp	Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Glu	Glu	Leu	
69					115					120					125		
71	caa	gta	gat	ttc	ctg	gat	cat	gtt	ccc	ctc	aca	aca	cac	aac	ttt	gct	555
72	Gln	Val	Asp	Phe	Leu	Asp	His	Val	Pro	Leu	Thr	Thr	His	Asn	Phe	Ala	
73				130					135					140			
75	cgg	aag	acg	ttc	ctg	aag	ctt	gcc	ttc	tgt	gac	atc	tgt	cag	aaa	ttc	603
76	Arg	Lys	Thr	Phe	Leu	Lys	Leu	Ala	Phe	Cys	Asp	Ile	Cys	Gln	Lys	Phe	
77			145					150					155				
79	ctg	ctc	aat	gga	ttt	cga	tgt	cag	act	tgt	ggc	tac	aaa	ttt	cat	gag	651
80	Leu	Leu	Asn	Gly	Phe	Arg	Cys	Gln	Thr	Cys	Gly	Tyr	Lys	Phe	His	Glu	
81		160					165					170					
83	cac	tgt	agc	acc	aaa	gta	cct	act	atg	tgt	gtg	gac	tgg	agt	aac	atc	699
84	His	Cys	Ser	Thr	Lys	Val	Pro	Thr	Met	Cys	Val	Asp	Trp	Ser	Asn	Ile	
85	175				180					185					190		
87	aga	caa	ctc	tta	ttg	ttt	cca	aat	tcc	act	att	ggg	gat	agt	gga	gtc	747
88	Arg	Gln	Leu	Leu	Leu	Phe	Pro	Asn	Ser	Thr	Ile	Gly	Asp	Ser	Gly	Val	
89				195					200					205			
91	cca	gca	cta	cct	tct	ttg	act	atg	cgt	cgt	atg	cga	gag	tct	gtt	tcc	795
92	Pro	Ala	Leu	Pro	Ser	Leu	Thr	Met	Arg	Arg	Met	Arg	Glu	Ser	Val	Ser	
93			210					215					220				
95	agg	atg	cct	gtt	agt	tct	cag	cac	aga	tat	tct	aca	cct	cac	gcc	ttc	843
96	Arg	Met	Pro	Val	Ser	Ser	Gln	His	Arg	Tyr	Ser	Thr	Pro	His	Ala	Phe	
97			225				230					235					
99	acc	ttt	aac	acc	tcc	agt	ccc	tca	tct	gaa	ggg	tcc	ctc	tcc	cag	agg	891
100	Thr	Phe	Asn	Thr	Ser	Ser	Pro	Ser	Ser	Glu	Gly	Ser	Leu	Ser	Gln	Arg	
101		240					245					250					
103	cag	agg	tcg	aca	tcc	aca	cct	aat	gtc	cac	atg	gtc	agc	acc	acg	ctg	939
104	Gln	Arg	Ser	Thr	Ser	Thr	Pro	Asn	Val	His	Met	Val	Ser	Thr	Thr	Leu	
105	255				260					265					270		
107	cct	gtg	gac	agc	agg	atg	att	gag	gat	gca	att	cga	agt	cac	agc	gaa	987
108	Pro	Val	Asp	Ser	Arg	Met	Ile	Glu	Asp	Ala	Ile	Arg	Ser	His	Ser	Glu	
109				275					280					285			
111	tca	gcc	tca	cct	tca	gcc	ctg	tcc	agt	agc	ccc	aac	aat	ctg	agc	cca	1035
112	Ser	Ala	Ser	Pro	Ser	Ala	Leu	Ser	Ser	Pro	Asn	Asn	Leu	Ser	Pro		
113			290					295					300				
115	aca	ggc	tgg	tca	cag	ccg	aaa	acc	ccc	gtg	cca	gca	caa	aga	gag	cgg	1083
116	Thr	Gly	Trp	Ser	Gln	Pro	Lys	Thr	Pro	Val	Pro	Ala	Gln	Arg	Glu	Arg	
117			305				310					315					
119	gca	cca	gta	tct	ggg	acc	cag	gag	aaa	aac	aaa	att	agg	cct	cgt	gga	1131
120	Ala	Pro	Val	Ser	Gly	Thr	Gln	Glu	Lys	Asn	Lys	Ile	Arg	Pro	Arg	Gly	
121			320				325					330					
123	cag	aga	gat	tca	agc	tat	tat	tgg	gaa	ata	gaa	gcc	agt	gaa	gtg	atg	1179
124	Gln	Arg	Asp	Ser	Ser	Tyr	Tyr	Trp	Glu	Ile	Glu	Ala	Ser	Glu	Val	Met	
125	335				340					345					350		
127	ctg	tcc	act	cgg	att	ggg	tca	ggc	tct	ttt	gga	act	gtt	tat	aag	ggg	1227
128	Leu	Ser	Thr	Arg	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	Lys	Gly	

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129		355		360		365	
131	aaa tgg cac	gga gat gtt gca gta aag atc cta aag gtt gtc gac cca	1275				
132	Lys Trp His	Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro					
133		370 375 380					
135	acc cca gag	caa ttc cag gcc ttc agg aat gag gtg gct gtt ctg cgc	1323				
136	Thr Pro Glu	Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg					
137		385 390 395					
139	aaa aca cgg	cat gtg aac att ctg ctt ttc atg ggg tac atg aca aag	1371				
140	Lys Thr Arg	His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys					
141		400 405 410					
143	gac aac ctg	gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac	1419				
144	Asp Asn Leu	Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr					
145	415	420 425 430					
147	aaa cac ctg	cat gtc cag gag acc aag ttt cag atg ttc cag cta att	1467				
148	Lys His Leu	His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile					
149		435 440 445					
151	gac att gcc	cgg cag acg gct cag gga atg gac tat ttg cat gca aag	1515				
152	Asp Ile Ala	Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys					
153		450 455 460					
155	aac atc atc	cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa	1563				
156	Asn Ile Ile	His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu					
157		465 470 475					
159	ggc tta aca	gtg aaa att gga gat ttt ggt ttg gca aca gta aag tca	1611				
160	Gly Leu Thr	Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser					
161		480 485 490					
163	cgc tgg agt	ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc	1659				
164	Arg Trp Ser	Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu					
165	495	500 505 510					
167	tgg atg gcc	cca gag gtg atc cga atg cag gat aac aac cca ttc agt	1707				
168	Trp Met Ala	Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser					
169		515 520 525					
171	ttc cag tcg	gat gtc tac tcc tat ggc atc gta ttg tat gaa ctg atg	1755				
172	Phe Gln Ser	Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met					
173		530 535 540					
175	acg ggg gag	ctt cct tat tct cac atc aac aac cga gat cag atc atc	1803				
176	Thr Gly Glu	Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile					
177		545 550 555					
179	ttc atg gtg	ggc cga gga tat gcc tcc cca gat ctt agt aag cta tat	1851				
180	Phe Met Val	Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr					
181		560 565 570					
183	aag aac tgc	ccc aaa gca atg aag agg ctg gta gct gac tgt gtg aag	1899				
184	Lys Asn Cys	Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys					
185	575	580 585 590					
187	aaa gta aag	gaa gag agg cct ctt ttt ccc cag atc ctg tct tcc att	1947				
188	Lys Val Lys	Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile					
189		595 600 605					
191	gag ctg ctc	caa cac tct cta ccg aag atc aac cgg agc gct tcc gag	1995				
192	Glu Leu Leu	Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu					
193		610 615 620					

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196 Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr
197      625      630      635
199 ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacctgtc 2093
200 Leu Thr Thr Ser Pro Arg Leu Pro Val Phe
201      640      645
203 ttcaggctgc caggggagga ggagaagcca gcaggcacca cttttctgct ccctttctcc 2153
204 agaggcagaa cacatgtttt cagagaagct ctgctaagga ccttctagac tgctcacagg 2213
205 gccttaactt catgttgctt tcttttctat ccctttgggc cctgggagaa ggaagccatt 2273
206 tgcagtgtct gtgtgtcctg ctccctcccc acattcccca tgctcaaggc ccagccttct 2333
207 gtagatgcgc aagtggatgt tgatgtagt acaaaaagca ggggcccgag cccagctgtt 2393
208 ggctacatga gtatttagag gaagtaaggt agcaggcagt ccagccctga tgtggagaca 2453
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215 acaaacagcc ttgtttctct agtcacatca tgtgtataca aggaagccag gaatacaggt 2873
216 tttcttgatg atttgggttt taattttgtt tttattgcac ctgacaaaat acagttatct 2933
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220 <211> LENGTH: 648
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226 1 5 10 15
227 Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
228 20 25 30
229 Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
230 35 40 45
231 Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
232 50 55 60
233 Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
234 65 70 75 80
235 Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
236 85 90 95
237 Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
238 100 105 110
239 Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
240 115 120 125
241 Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
242 130 135 140
243 Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
244 145 150 155 160
245 Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
246 165 170 175
247 Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln

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248		180		185		190	
249	Leu	Leu	Leu	Phe	Pro	Asn	Ser
250			195			200	
251	Leu	Pro	Ser	Leu	Thr	Met	Arg
252		210				215	
253	Pro	Val	Ser	Ser	Gln	His	Arg
254	225				230		
255	Asn	Thr	Ser	Ser	Pro	Ser	Ser
256				245		250	
257	Ser	Thr	Ser	Thr	Pro	Asn	Val
258			260			265	
259	Asp	Ser	Arg	Met	Ile	Glu	Asp
260			275			280	
261	Ser	Pro	Ser	Ala	Leu	Ser	Ser
262		290				295	
263	Trp	Ser	Gln	Pro	Lys	Thr	Pro
264	305				310		
265	Val	Ser	Gly	Thr	Gln	Glu	Lys
266				325		330	
267	Asp	Ser	Ser	Tyr	Trp	Glu	Ile
268			340			345	
269	Thr	Arg	Ile	Gly	Ser	Gly	Ser
270			355			360	
271	His	Gly	Asp	Val	Ala	Val	Lys
272		370				375	
273	Glu	Gln	Phe	Gln	Ala	Phe	Arg
274	385				390		
275	Arg	His	Val	Asn	Ile	Leu	Leu
276				405		410	
277	Leu	Ala	Ile	Val	Thr	Gln	Trp
278			420			425	
279	Leu	His	Val	Gln	Glu	Thr	Lys
280			435			440	
281	Ala	Arg	Gln	Thr	Ala	Gln	Gly
282		450				455	
283	Ile	His	Arg	Asp	Met	Lys	Ser
284	465				470		
285	Thr	Val	Lys	Ile	Gly	Asp	Phe
286				485		490	
287	Ser	Gly	Ser	Gln	Gln	Val	Glu
288			500			505	
289	Ala	Pro	Glu	Val	Ile	Arg	Met
290			515			520	
291	Ser	Asp	Val	Tyr	Ser	Tyr	Gly
292		530				535	
293	Glu	Leu	Pro	Tyr	Ser	His	Ile
294	545				550		
295	Val	Gly	Arg	Gly	Tyr	Ala	Ser
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VERIFICATION SUMMARY

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Input Set : A:\TSRI7102Seq-list.TXT

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L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:533 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:536 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6